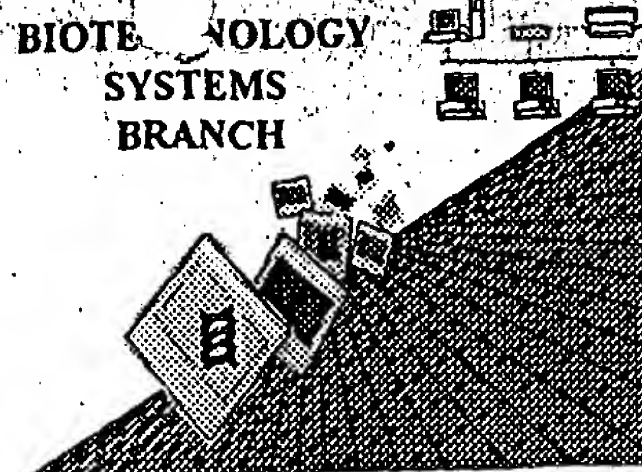


## **RAW SEQUENCE LISTING ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/873,106

Source: OIPE

Date Processed by STIC: 6-20-01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,106

DATE: 06/20/2001

TIME: 12:29:35

Input Set : A:\1062.1021-004.TXT

Output Set: N:\CRF3\06202001\I873106.raw

4 <110> APPLICANT: Reinherz, Ellis L.  
 5 Freund, Christian  
 6 Li, Jing  
 7 Nishizawa, Kazuhisa  
 8 Wagner, Gerhard  
 10 <120> TITLE OF INVENTION: Cloning and Characterization of a CD2  
 11 Binding Protein (CD2BP2)  
 14 <130> FILE REFERENCE: 1062.1021-004  
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/873,106  
 C--> 16 <141> CURRENT FILING DATE: 2001-06-01  
 16 <150> PRIOR APPLICATION NUMBER: US 60/111,007  
 17 <151> PRIOR FILING DATE: 1998-12-04  
 19 <150> PRIOR APPLICATION NUMBER: US 60/115,647  
 20 <151> PRIOR FILING DATE: 1999-01-13  
 22 <150> PRIOR APPLICATION NUMBER: PCT/US99/26993  
 23 <151> PRIOR FILING DATE: 1999-11-15  
 25 <160> NUMBER OF SEQ ID NOS: 25  
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply  
 Corrected Diskette Needed  
 pp 2-8  
 The format  
 errors shown  
 were corrected.

## ERRORED SEQUENCES

132 <210> SEQ ID NO: 2  
 133 <211> LENGTH: 341  
 134 <212> TYPE: PRT  
 135 <213> ORGANISM: Homo sapiens  
 137 <400> SEQUENCE: 2  
 138 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp  
 139 1 5 10 15  
 140 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala  
 141 20 25 30  
 142 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp  
 143 35 40 45  
 144 Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp  
 145 50 55 60  
 146 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro  
 147 65 70 75 80  
 148 Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met  
 149 85 90 95  
 150 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp  
 151 100 105 110  
 152 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile  
 153 115 120 125  
 154 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu  
 155 130 135 140  
 156 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly  
 157 145 150 155 160

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/873,106

DATE: 06/20/2001  
TIME: 12:29:35

Input Set : A:\1062.1021-004.TXT  
Output Set: N:\CRF3\06202001\I873106.raw

158 Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg  
159 165 170 175  
160 Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln  
161 180 185 190  
162 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln  
163 195 200 205  
164 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg  
165 210 215 220  
166 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His  
167 225 230 235 240  
168 Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala  
169 245 250 255  
170 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu  
171 260 265 270  
172 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu  
173 275 280 285  
174 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met  
175 290 295 300  
176 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg

E--> 177

305 310 315 320 Lys Leu Asp Pro Pro Gly Gly Gln

179 <210> SEQ ID NO: 3  
180 <211> LENGTH: 26  
181 <212> TYPE: PRT  
182 <213> ORGANISM: Homo sapiens  
184 <400> SEQUENCE: 3

E--> 185

Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr 1

187 <210> SEQ ID NO: 4  
188 <211> LENGTH: 27  
189 <212> TYPE: PRT  
190 <213> ORGANISM: Caenorhabditis elegans  
192 <400> SEQUENCE: 4

E--> 193

Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu 1

195 <210> SEQ ID NO: 5  
196 <211> LENGTH: 27  
197 <212> TYPE: PRT  
198 <213> ORGANISM: Caenorhabditis elegans  
200 <400> SEQUENCE: 5

E--> 201

Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn 1

203 <210> SEQ ID NO: 6  
204 <211> LENGTH: 27  
205 <212> TYPE: PRT  
206 <213> ORGANISM: Caenorhabditis elegans  
208 <400> SEQUENCE: 6

E--> 209

Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu 1

211 <210> SEQ ID NO: 7  
212 <211> LENGTH: 29  
213 <212> TYPE: PRT  
214 <213> ORGANISM: Saccharomyces cerevisiae

5  
5  
5  
Format  
error  
causing  
misaligned  
amino  
acids and  
amino acid  
numbers.

216 <400> SEQUENCE: 7

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,106

DATE: 06/20/2001

TIME: 12:29:35

Input Set : A:\1062.1021-004.TXT

Output Set: N:\CRF3\06202001\I873106.raw

E--&gt; 217

Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser 1

219 &lt;210&gt; SEQ ID NO: 8

220 &lt;211&gt; LENGTH: 27

221 &lt;212&gt; TYPE: PRT

222 &lt;213&gt; ORGANISM: Saccharomyces cerevisiae

224 &lt;400&gt; SEQUENCE: 8

5

Same

E--&gt; 225

Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser 1

227 &lt;210&gt; SEQ ID NO: 9

228 &lt;211&gt; LENGTH: 17

229 &lt;212&gt; TYPE: PRT

230 &lt;213&gt; ORGANISM: Artificial Sequence

232 &lt;220&gt; FEATURE:

233 &lt;223&gt; OTHER INFORMATION: Motif in CD2 binding region of CD2BP2

236 &lt;221&gt; NAME/KEY: VARIANT

237 &lt;222&gt; LOCATION: (1)...(2)

238 &lt;223&gt; OTHER INFORMATION: Xaa = Any Amino Acid

240 &lt;221&gt; NAME/KEY: VARIANT

241 &lt;222&gt; LOCATION: (3)...(3)

242 &lt;223&gt; OTHER INFORMATION: Xaa can be Tyr or Phe

244 &lt;221&gt; NAME/KEY: VARIANT

245 &lt;222&gt; LOCATION: (4)...(7)

246 &lt;223&gt; OTHER INFORMATION: Xaa = Any Amino Acid

248 &lt;221&gt; NAME/KEY: VARIANT

249 &lt;222&gt; LOCATION: (8)...(8)

250 &lt;223&gt; OTHER INFORMATION: Xaa can be Met or Val

252 &lt;221&gt; NAME/KEY: VARIANT

253 &lt;222&gt; LOCATION: (9)...(15)

254 &lt;223&gt; OTHER INFORMATION: Xaa = Any Amino Acid

256 &lt;400&gt; SEQUENCE: 9

5

E--&gt; 257

Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Thr 1

259 &lt;210&gt; SEQ ID NO: 10

260 &lt;211&gt; LENGTH: 6

261 &lt;212&gt; TYPE: PRT

262 &lt;213&gt; ORGANISM: Artificial Sequence

264 &lt;220&gt; FEATURE:

265 &lt;223&gt; OTHER INFORMATION: CD2BP2 binding region

268 &lt;400&gt; SEQUENCE: 10

5

Same

E--&gt; 269 Pro Pro Pro Gly His Arg 1

5

271 &lt;210&gt; SEQ ID NO: 11

272 &lt;211&gt; LENGTH: 70

273 &lt;212&gt; TYPE: PRT

274 &lt;213&gt; ORGANISM: Homo sapiens

276 &lt;400&gt; SEQUENCE: 11

277 Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro

278 1 5 10 15

279 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro

280 20 25 30

281 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro

E--&gt; 282

35

40

45

Arg Pro Arg Val Gln Pro Lys Pro

Same

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,106

DATE: 06/20/2001

TIME: 12:29:35

Input Set : A:\1062.1021-004.TXT

Output Set: N:\CRF3\06202001\I873106.raw

306 <210> SEQ ID NO: 14  
307 <211> LENGTH: 8  
308 <212> TYPE: PRT  
309 <213> ORGANISM: Artificial Sequence  
311 <220> FEATURE:  
312 <223> OTHER INFORMATION: Flag Epitope  
314 <400> SEQUENCE: 14

E--&gt; 315 Asp Tyr Lys Asp Asp Asp Asp Lys 1

5

317 <210> SEQ ID NO: 15  
318 <211> LENGTH: 31  
319 <212> TYPE: PRT  
320 <213> ORGANISM: Gallus gallus  
322 <220> FEATURE:  
323 <223> OTHER INFORMATION: Flag Epitope  
325 <400> SEQUENCE: 15

E--&gt; 326

Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Ser Asn 1

5

328 <210> SEQ ID NO: 16  
329 <211> LENGTH: 38  
330 <212> TYPE: PRT  
331 <213> ORGANISM: Drosophila melanogaster  
333 <220> FEATURE:  
334 <223> OTHER INFORMATION: Flag Epitope  
336 <400> SEQUENCE: 16  
337 Glu Val Thr Trp Glu Phe Lys Trp Ser Gln Asp Glu Thr Asp Ile Gln

E--&gt; 338

1 5 10 15 Gly Pro Phe Ser Thr Glu Lys Met

340 <210> SEQ ID NO: 17  
341 <211> LENGTH: 34  
342 <212> TYPE: PRT  
343 <213> ORGANISM: Leishmania major  
345 <220> FEATURE:  
346 <223> OTHER INFORMATION: Flag Epitope  
348 <400> SEQUENCE: 17  
349 Val Trp Met Met Arg Trp Lys Ala Lys Pro Thr Val Gln His Gly Pro

E--&gt; 350

1 5 10 15 Phe Thr Asp Asp Ala Ile Gln Gln

352 <210> SEQ ID NO: 18  
353 <211> LENGTH: 36  
354 <212> TYPE: PRT  
355 <213> ORGANISM: Caenorhabditis elegans  
357 <220> FEATURE:  
358 <223> OTHER INFORMATION: Flag Epitope  
360 <400> SEQUENCE: 18  
361 Val Ile Asp Thr Lys Trp His Tyr Leu Gly Pro Asp Ser Glu Lys Tyr

E--&gt; 362

1 5 10 15 Gly Pro Tyr Met Ser Lys Asp Met

364 <210> SEQ ID NO: 19  
365 <211> LENGTH: 35  
366 <212> TYPE: PRT  
367 <213> ORGANISM: Caenorhabditis elegans  
369 <220> FEATURE:  
370 <223> OTHER INFORMATION: Flag Epitope

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,106

DATE: 06/20/2001

TIME: 12:29:35

Input Set : A:\1062.1021-004.TXT

Output Set: N:\CRF3\06202001\I873106.raw

372 &lt;400&gt; SEQUENCE: 19

373 Val Glu Ser Ser Trp Arg Tyr Ile Asp Thr Gln Gly Gln Ile His Gly

E--&gt; 374

1 5 10 15 Pro Phe Thr Ile Gln Met Met Ser

376 &lt;210&gt; SEQ ID NO: 20

377 &lt;211&gt; LENGTH: 35

378 &lt;212&gt; TYPE: PRT

379 &lt;213&gt; ORGANISM: Saccharomyces cerevisiae

381 &lt;220&gt; FEATURE:

382 &lt;223&gt; OTHER INFORMATION: Flag Epitope

384 &lt;400&gt; SEQUENCE: 20

385 Ile Glu Ser Gln Trp Lys Tyr Ile Asp Ser Asn Gly Asn Ile Gln Gly

E--&gt; 386

1 5 10 15 Pro Phe Gly Thr Asn Asn Met Ser

388 &lt;210&gt; SEQ ID NO: 21

389 &lt;211&gt; LENGTH: 31

390 &lt;212&gt; TYPE: PRT

391 &lt;213&gt; ORGANISM: Saccharomces pombe

393 &lt;220&gt; FEATURE:

394 &lt;223&gt; OTHER INFORMATION: Flag Epitope

396 &lt;400&gt; SEQUENCE: 21

E--&gt; 397

Trp Leu Tyr Lys Asp Pro Gln Asn Asn Val Gln Gly Pro Phe Thr Gly 1

5

399 &lt;210&gt; SEQ ID NO: 22

400 &lt;211&gt; LENGTH: 21

401 &lt;212&gt; TYPE: PRT

402 &lt;213&gt; ORGANISM: Homo sapiens

404 &lt;220&gt; FEATURE:

405 &lt;223&gt; OTHER INFORMATION: Flag Epitope

407 &lt;400&gt; SEQUENCE: 22

E--&gt; 408

Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro 1

5

410 &lt;210&gt; SEQ ID NO: 23

411 &lt;211&gt; LENGTH: 62

412 &lt;212&gt; TYPE: PRT

413 &lt;213&gt; ORGANISM: Homo sapiens

415 &lt;220&gt; FEATURE:

416 &lt;223&gt; OTHER INFORMATION: Flag Epitope

418 &lt;400&gt; SEQUENCE: 23

419 Asp Val Met Trp Glu Tyr Lys Trp Glu Asn Thr Gly Asp Ala Glu Leu

420 1 5 10 15

421 Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr Trp Val Ser Glu Gly

422 20 25 30

E--&gt; 423

Tyr Phe Pro Asp Gly Val Tyr Cys Arg Lys Leu Asp Pro Pro Gly Gly

35

40

425 &lt;210&gt; SEQ ID NO: 24

426 &lt;211&gt; LENGTH: 31

427 &lt;212&gt; TYPE: PRT

428 &lt;213&gt; ORGANISM: Homo sapiens

430 &lt;220&gt; FEATURE:

431 &lt;223&gt; OTHER INFORMATION: Flag Epitope

433 &lt;400&gt; SEQUENCE: 24

E--&gt; 434

Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Asn Asn 1  
436 <210> SEQ ID NO: 25

5



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,106

DATE: 06/20/2001

TIME: 12:29:35

Input Set : A:\1062.1021-004.TXT

Output Set: N:\CRF3\06202001\I873106.raw

437 <211> LENGTH: 31

438 <212> TYPE: PRT

439 <213> ORGANISM: Homo sapiens

441 <220> FEATURE:

442 <223> OTHER INFORMATION: Flag Epitope

444 <400> SEQUENCE: 25

*Same*

E--> 445

Gln Trp Phe Ser Arg Ser Leu Ala Pro Cys Pro Gly Pro Phe Thr Thr 1

5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/873,106

DATE: 06/20/2001

TIME: 12:29:36

Input Set : A:\1062.1021-004.TXT

Output Set: N:\CRF3\06202001\I873106.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:177 M:252 E: No. of Seq. differs, <211>LENGTH:Input:341 Found:320 SEQ:2  
 L:185 M:252 E: No. of Seq. differs, <211>LENGTH:Input:26 Found:0 SEQ:3  
 L:193 M:252 E: No. of Seq. differs, <211>LENGTH:Input:27 Found:0 SEQ:4  
 L:201 M:252 E: No. of Seq. differs, <211>LENGTH:Input:27 Found:0 SEQ:5  
 L:209 M:252 E: No. of Seq. differs, <211>LENGTH:Input:27 Found:0 SEQ:6  
 L:217 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:225 M:252 E: No. of Seq. differs, <211>LENGTH:Input:27 Found:0 SEQ:8  
 L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
 L:257 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:269 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:10  
 L:282 M:252 E: No. of Seq. differs, <211>LENGTH:Input:70 Found:48 SEQ:11  
 L:315 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:14  
 L:326 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:338 M:252 E: No. of Seq. differs, <211>LENGTH:Input:38 Found:16 SEQ:16  
 L:350 M:252 E: No. of Seq. differs, <211>LENGTH:Input:34 Found:16 SEQ:17  
 L:362 M:252 E: No. of Seq. differs, <211>LENGTH:Input:36 Found:16 SEQ:18  
 L:374 M:252 E: No. of Seq. differs, <211>LENGTH:Input:35 Found:16 SEQ:19  
 L:386 M:252 E: No. of Seq. differs, <211>LENGTH:Input:35 Found:16 SEQ:20  
 L:397 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:408 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:0 SEQ:22  
 L:423 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:32 SEQ:23  
 L:434 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:445 M:333 E: Wrong sequence grouping, Amino acids not in groups!